

Evaluation of King et al 2006, "Comprehensive Analysis of Molecular Phylogeographic Structure Among Meadow Jumping Mice (*Zapus hudsonius*) Reveals Evolutionarily Distinct Subspecies"

Mary Ashley
Department of Biological Sciences
University of Illinois at Chicago
Chicago, IL 60607

1) Please analyze the techniques used . . .

This is a thorough study that employs 21 microsatellite loci and approximately 1380 bp of mitochondrial DNA, including control region and cytochrome b. Sample sizes are large and representative. The genetic data appear to be technically sound. The analyses are thorough and appropriate. Overall, this is a very convincing study.

2) Based on the data presented in the report, do you support the authors' conclusions about the taxonomic validity of *Z. h. preblei* and neighboring subspecies?

Yes, the authors make a strong case. The conclusion that *Z. h. preblei* and other subspecies represent distinct evolutionary lineages is consistently supported by the data. Among the most convincing evidence, for me, include the finding that there were no shared mitochondrial haplotypes among subspecies, the results of the statistical parsimony analysis for mtDNA, and the results of the *structure* analysis for the microsatellite data.

3) Based on the data presented in the report, do you support the authors' conclusions that *Z. h. preblei* is comprised of at least two distinct population segments worthy of individual management consideration?

The microsatellite *structure* analysis, in particular, provides evidence for population structure within the *Z. h. preblei* subspecies, corresponding to a northern and southern populations. The mtDNA sequences do not provide much additional support for this conclusion. Overall the analysis indicates that the north and south collections are genetically more similar to each other than to other subspecies, but with some impediments to gene flow within the subspecies.

4) Are there possible alternative interpretations of the data . . .?

None that seem very likely. The only possible problem with the interpretation is the lack of reciprocal monophyly in the mtDNA phylogenetic analysis. However, the lack of shared haplotypes among subspecies, the results of the statistical parsimony, and the additional support from nuclear microsatellite loci to me trumps the issue of reciprocal monophyly.

5) What additional analysis, if any, is needed to verify the study's assertions and why?

The genetic analysis to me now seems rather complete. Perhaps more sampling within *Z. h. preblei* would help clarify the status of evolutionary lineages within the subspecies. Overall, the data that I see is most lacking with regards to conservation and protection is would be ecological and demographic data including habitat requirements and responses to habitat alterations.

6) The conclusions of Ramey et al. (2005) and King et al. (2006) would appear to conflict

...

It is surprising to me that these two studies, which used similar approaches for the genetic work, came to such strikingly different conclusions. I do not know the complete explanation for this conflict. The data collection and analyses in both studies seemed to be technically sound. My best guess is that the conclusions of Ramey et al. were based much too heavily on a few questionable museum specimens rather than more recent field collections (a point I brought up in an earlier review). I would also point to the sampling for the microsatellite study in King et al. was much more appropriate than that of Ramey et al., both in terms of population sampling and number of loci assayed. I believe these two factors contributed more to the conflicting conclusions than specifics of data analyses. I previously felt that conclusions of the Ramey et al. study were premature, and was not in favor of synonymizing the subspecies at that point. I feel that King et al. have shown convincingly that such synonymy is not warranted.